CLAIM AMENDMENTS

Please amend claims 1 and 12 as follows.

1. (Currently Amended) A composition comprising a plurality of cDNAs that are differentially expressed in a liver disorder and selected from SEQ ID NOs:~~1-401~~1-5, 7, 9-10, 12-14, 16, 18, 20, 22-26, 28, 30, 32, 34, 36-39, 41, 43-46, 48-49, 51-57, 59-61, 63, 65, 67, 69-72, 74-75, 77, 79-82, 84-85, 87-92, 94, 96-101, 103-104, 106-108, 110-117, 119-120, 122, 124-126, 128-129, 131, 133, 135-137, 139-140, 142, 144-145, 147-148, 150-153, 155-157, 159--162, 164, 166-177, 179, 181-183, 185-186, 188-191, 193-194, 196, 198-199, 201, 203, 205-206, 208, 210-221, 223-224, 226-227, 229-231, 233-234, 236-241, 243-244, 246, 248-257, 259, 261-269, 271, 273-274, 276-277, 279-284, 286-290, 292-295, 297, 299, 301-308, 310, 312, 314-317, 319-323, 325-330, 332, 334-335, 337-342, 344-347, 349-359,, 361-366, 368-369, 371-377, 379-389, and 391-401, or their complements.

2. (Original) The composition of claim 1, wherein each of the cDNAs is downregulated at least two-fold and is selected from SEQ ID NOs:3, 32, 94, 99, 100, 108, 137, 196, 274, 299, 380.

3. (Original) The composition of claim 1, wherein each of the cDNAs is upregulated at least two-fold and is selected from SEQ ID NOs:9, 10, 70, 144, 145, 147, 164, 186, 190, 191, 203, 271, 305, 344.

4. (Original) The composition of claim 1, wherein the liver disorder is hyperlipidemia.

5. (Original) The composition of claim 1, wherein the liver disorder is selected from hyperlipidemia, hypertension, type II diabetes, tumors of the liver, and disorders of the inflammatory and immune response.

6. (Original) The composition of claim 1, wherein the cDNAs are immobilized on a substrate.

7. (Original) A high throughput method for detecting differential expression of one or more cDNAs in a sample containing nucleic acids, the method comprising:

(a) hybridizing the substrate of claim 6 with nucleic acids of the sample, thereby forming one or more hybridization complexes;

(b) detecting the hybridization complexes; and

(c) comparing the hybridization complexes with those of a standard, wherein differences between the standard and sample hybridization complexes indicate differential expression of cDNAs in the sample.

8. (Original) The method of claim 7, where in the nucleic acids of the sample are amplified prior to hybridization.

9. (Original) The method of claim 6, wherein the sample is from a subject with Alzheimer's disease and comparison with a standard defines an early, mid, or late stage of that disease.

10. (Original) A high throughput method of screening a plurality of molecules or compounds to identify a ligand which specifically binds a cDNA, the method comprising:

(a) combining the composition of claim 1 with the plurality of molecules or compounds under conditions to allow specific binding; and

(b) detecting specific binding between each cDNA and at least one molecule or compound, thereby identifying a ligand that specifically binds to each cDNA.

11. (Original) The method of claim 10 wherein the plurality of molecules or compounds are selected from DNA molecules, RNA molecules, peptide nucleic acid molecules, mimetics, peptides, transcription factors, repressors, and regulatory proteins.

12. (Currently Amended) An isolated cDNA selected from SEQ ID NOs:23, 32, 56, 59, 97, 136, 155, 157, 186, 226, 255, 264, 303, 308, 310, 323, 330, 353, 354, 364, 395.

13. (Original) A vector containing the cDNA of claim 12.

14. (Original) A host cell containing the vector of claim 13.

15. (Original) A method for producing a protein, the method comprising the steps of:

(a) culturing the host cell of claim 14 under conditions for expression of protein; and

(b) recovering the protein from the host cell culture.

16. (Original) A protein or a portion thereof produced by the method of claim 15.

17. (Original) A high-throughput method for using a protein to screen a plurality of molecules or compounds to identify at least one ligand which specifically binds the protein, the method comprising:

(a) combining the protein of claim 16 with the plurality of molecules or compounds under conditions to allow specific binding; and

(b) detecting specific binding between the protein and a molecule or compound, thereby identifying a ligand which specifically binds the protein.

18. (Original) The method of claim 17 wherein the plurality of molecules or compounds is selected from DNA molecules, RNA molecules, peptide nucleic acid molecules, mimetics, peptides, proteins, agonists, antagonists, antibodies or their fragments, immunoglobulins, inhibitors, drug compounds, and pharmaceutical agents.

19. (Original) A method of using a protein to produce an antibody, the method comprising:

a) immunizing an animal with the protein of claim 16 under conditions to elicit an antibody response;

b) isolating animal antibodies; and

c) screening the isolated antibodies with the protein, thereby identifying an antibody which specifically binds the protein.

20. (Original) A method of purifying an antibody, the method comprising:

a) combining the protein of claim 16 with a sample under conditions to allow specific binding;

b) recovering the bound protein; and

c) separating the protein from the antibody, thereby obtaining purified antibody.

21. (Original) An isolated protein selected from SEQ ID NOs:158, 311, 331.